Helms

#12

RAW SEQUENCE LISTING   DATE: 05/21/2001
PATENT APPLICATION: US/09/381,497A   TIME: 11:16:56

Input Set : A:\-317-1.app
Output Set: N:\CRF3\05212001\I381497A.raw

SEQUENCE LISTING

ENTERED

```
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: FitzGerald, David
 7                     Pastan, Ira
 8                     Mansfield, Elizabeth
 9                     Kreitman, Robert
11     (ii) TITLE OF INVENTION: Recombinant Antibodies and
12                              Immunoconjugates Targeted to CD-22 Bearing Cells and
13                              Tumors
15    (iii) NUMBER OF SEQUENCES: 15
17     (iv) CORRESPONDENCE ADDRESS:
18          (A) ADDRESSEE: Townsend and Townsend and Crew LLP
19          (B) STREET: Two Embarcadero Center, Eighth Floor
20          (C) CITY: San Francisco
21          (D) STATE: California
22          (E) COUNTRY: USA
23          (F) ZIP: 94111-3834
25      (v) COMPUTER READABLE FORM:
26          (A) MEDIUM TYPE: Floppy disk
27          (B) COMPUTER: IBM PC compatible
28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31     (vi) CURRENT APPLICATION DATA:
C--> 32          (A) APPLICATION NUMBER: US/09/381,497A
C--> 33          (B) FILING DATE: 21-May-2001
34          (C) CLASSIFICATION:
40    (vii) PRIOR APPLICATION DATA:
37          (A) APPLICATION NUMBER: WO PCT/US98/05453
38          (B) FILING DATE: 19-MAR-1998
41          (A) APPLICATION NUMBER: US 60/041,437
42          (B) FILING DATE: 20-MAR-1997
44   (viii) ATTORNEY/AGENT INFORMATION:
45          (A) NAME: Weber, Ellen Lauver
46          (B) REGISTRATION NUMBER: 32,762
47          (C) REFERENCE/DOCKET NUMBER: 015280-317100US
49     (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: (415) 576-0200
51          (B) TELEFAX: (415) 576-0300
54 (2) INFORMATION FOR SEQ ID NO: 1:
56      (i) SEQUENCE CHARACTERISTICS:
57          (A) LENGTH: 369 base pairs
58          (B) TYPE: nucleic acid
59          (C) STRANDEDNESS: single
60          (D) TOPOLOGY: linear
W--> 62     (ii) MOLECULE TYPE: DNA
65     (ix) FEATURE:
66          (A) NAME/KEY: CDS
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67             (B) LOCATION: 1..369
68             (D) OTHER INFORMATION: /product= "RFB4 heavy chain"
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA GGG       48
74 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
75  1               5                   10                  15
77 TCC CTG AAA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT ATC TAT       96
78 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
79             20                  25                  30
81 GAC ATG TCT TGG GTT CGC CAG ACT CCG GAG AAG AGG CTG GAG TGG GTC      144
82 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
83          35                  40                  45
85 GCA TAC ATT AGT AGT GGT GGT GGT ACC ACC TAC TAT CCA GAC ACT GTG      192
86 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
87          50                  55                  60
89 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTG TAC      240
90 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
91 65                  70                  75                  80
93 CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC ACA GCC ATG TAT TAC TGT      288
94 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
95             85                  90                  95
97 GCA AGA CAT AGT GGC TAC GGT AGT AGC TAC GGG GTT TTG TTT GCT TAC      336
98 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
99          100                 105                 110
101 TGG GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA                         369
102 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
103          115                 120
106 (2) INFORMATION FOR SEQ ID NO: 2:
108      (i) SEQUENCE CHARACTERISTICS:
109             (A) LENGTH: 123 amino acids
110             (B) TYPE: amino acid
111             (D) TOPOLOGY: linear
113      (ii) MOLECULE TYPE: protein
115      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
117 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
118  1               5                   10                  15
120 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
121             20                  25                  30
123 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
124          35                  40                  45
126 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
127          50                  55                  60
129 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
130 65                  70                  75                  80
132 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
133             85                  90                  95
135 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
136          100                 105                 110
138 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
```

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```
139          115               120
142 (2) INFORMATION FOR SEQ ID NO: 3:
144     (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 321 base pairs
146          (B) TYPE: nucleic acid
147          (C) STRANDEDNESS: single
148          (D) TOPOLOGY: linear
W--> 150    (ii) MOLECULE TYPE: DNA
153    (ix) FEATURE:
154          (A) NAME/KEY: CDS
155          (B) LOCATION: 1..321
156          (D) OTHER INFORMATION: /product= "RFB4 light chain"
159    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161 GAT ATC CAG ATG ACC CAG ACT ACA TCC TCC CTG TCT GCC TCT CTG GGA          48
162 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
163  1          5               10              15
165 GAC AGA GTC ACC ATT AGT TGC AGG GCA AGT CAG GAC ATT AGC AAT TAT          96
166 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
167          20              25              30
169 TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT AAA CTC CTG ATC          144
170 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
171          35              40              45
173 TAC TAC ACA TCA ATA TTA CAC TCA GGA GTC CCA TCA AGG TTC AGT GGC          192
174 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
175          50              55              60
177 AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC AAC CTG GAG CAA          240
178 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
179  65              70              75              80
181 GAA GAT TTT GCC ACT TAC TTT TGC CAA CAG GGT AAT ACG CTT CCG TGG          288
182 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
183              85              90              95
185 ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA                              321
186 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
187          100             105
190 (2) INFORMATION FOR SEQ ID NO: 4:
192     (i) SEQUENCE CHARACTERISTICS:
193          (A) LENGTH: 107 amino acids
194          (B) TYPE: amino acid
195          (D) TOPOLOGY: linear
197    (ii) MOLECULE TYPE: protein
199    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
201 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
202  1          5               10              15
204 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
205          20              25              30
207 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
208          35              40              45
210 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
211          50              55              60
```

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```
213 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
214 65                  70                  75                  80
216 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
217                 85                  90                  95
219 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
220                 100                 105
223 (2) INFORMATION FOR SEQ ID NO: 5:
225      (i) SEQUENCE CHARACTERISTICS:
226           (A) LENGTH: 4 amino acids
227           (B) TYPE: amino acid
228           (C) STRANDEDNESS:
229           (D) TOPOLOGY: linear
231      (ii) MOLECULE TYPE: peptide
234      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
236       Gly Gly Gly Ser
237       1
240 (2) INFORMATION FOR SEQ ID NO: 6:
242      (i) SEQUENCE CHARACTERISTICS:
243           (A) LENGTH: 33 base pairs
244           (B) TYPE: nucleic acid
245           (C) STRANDEDNESS: single·
246           (D) TOPOLOGY: linear
W--> 248      (ii) MOLECULE TYPE: DNA
251      (ix) FEATURE:
252           (A) NAME/KEY: -
253           (B) LOCATION: 1..33
254           (D) OTHER INFORMATION: /note= "RFB4 VH5 heavy chain primer"
257      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
259 GGACCTCATA TGGAAGTGCA GCTGGTGGAG TCT                                33
262 (2)·INFORMATION FOR SEQ ID NO: 7:
264      (i) SEQUENCE CHARACTERISTICS:
265           (A) LENGTH: 24 base pairs
266           (B) TYPE: nucleic acid
267           (C) STRANDEDNESS: single
268           (D) TOPOLOGY: linear
W--> 270      (ii) MOLECULE TYPE: DNA
273      (ix) FEATURE:
274           (A) NAME/KEY: -
275           (B) LOCATION: 1..24
276           (D) OTHER INFORMATION: /note= "gamma-CH1 heavy chain primer"
279      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
281 AGCAGATCCA GGGGCCAGTG GATA                                          24
284 (2) INFORMATION FOR SEQ ID NO: 8:
286      (i) SEQUENCE CHARACTERISTICS:
287           (A) LENGTH: 54 base pairs
288           (B) TYPE: nucleic acid
289           (C) STRANDEDNESS: single
290           (D) TOPOLOGY: linear
W--> 292      (ii) MOLECULE TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 05/21/2001
PATENT APPLICATION: US/09/381,497A   TIME: 11:16:57

Input Set : A:\-317-1.app
Output Set: N:\CRF3\05212001\I381497A.raw

```
295      (ix) FEATURE:
296           (A) NAME/KEY: -
297           (B) LOCATION: 1..54
298           (D) OTHER INFORMATION: /note= "RFB4 VH3 heavy chain primer"
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
303 AGATCCGCCA CCACCGGATC CGCCTCCGCC TGCAGAGACA GTGACCAGAG TCCC          54
306 (2) INFORMATION FOR SEQ ID NO: 9:
308      (i) SEQUENCE CHARACTERISTICS:
309           (A) LENGTH: 27 base pairs
310           (B) TYPE: nucleic acid
311           (C) STRANDEDNESS: single
312           (D) TOPOLOGY: linear
W--> 314     (ii) MOLECULE TYPE: DNA
317      (ix) FEATURE:
318           (A) NAME/KEY: -
319           (B) LOCATION: 1..27
320           (D) OTHER INFORMATION: /note= "RFB4 VH3 dsFv heavy chain
321 primer"
325      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
327 CCGGAAGCTT TTGCAGAGAC AGTGACC                                        27
330 (2) INFORMATION FOR SEQ ID NO: 10:
332      (i) SEQUENCE CHARACTERISTICS:
333           (A) LENGTH: 28 base pairs
334           (B) TYPE: nucleic acid
335           (C) STRANDEDNESS: single
336           (D) TOPOLOGY: linear
W--> 338     (ii) MOLECULE TYPE: DNA
341      (ix) FEATURE:
342           (A) NAME/KEY: -
343           (B) LOCATION: 1..28
344           (D) OTHER INFORMATION: /note= "RFB4 VH dsFv(cys) heavy chain
345 primer"
348      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
350 GACCCACTCC AGGCACTTCT CCGGAGTC                                       28
353 (2) INFORMATION FOR SEQ ID NO: 11:
355      (i) SEQUENCE CHARACTERISTICS:
356           (A) LENGTH: 48 base pairs
357           (B) TYPE: nucleic acid
358           (C) STRANDEDNESS: single
359           (D) TOPOLOGY: linear
W--> 361     (ii) MOLECULE TYPE: DNA
364      (ix) FEATURE:
365           (A) NAME/KEY: -
366           (B) LOCATION: 1..48
367           (D) OTHER INFORMATION: /note= "RFB4 VL5 light chain primer"
370      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
372 GGTGGCGGAT CTGGAGGTGG CGGAAGCGAT ATCCAGATGA CACAGACT               48
375 (2) INFORMATION FOR SEQ ID NO: 12:
377      (i) SEQUENCE CHARACTERISTICS:
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VERIFICATION SUMMARY   DATE: 05/21/2001
PATENT APPLICATION: US/09/381,497A   TIME: 11:16:58

Input Set : **A:\-317-1.app**
Output Set: **N:\CRF3\05212001\I381497A.raw**

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L:32  M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:62  M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:150 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:248 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:270 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:292 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:405 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:427 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:450 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
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